RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/641,149_

Source: _IFWO_

Date Processed by STIC: _3-30-05_

ENTERED

IFWO

RAW SEQUENCE LISTING   DATE: 03/30/2005
PATENT APPLICATION: **US/10/641,149**   TIME: 10:17:04

Input Set : **A:\028723-385.txt**
Output Set: **N:\CRF4\03302005\J641149.raw**

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 4 <110> APPLICANT: Tobin, Allan J.
 5        Erlander, Mark G.
 6        Kaufman, Daniel L.
 8 <120> TITLE OF INVENTION: Cloned Glumatic Acid Decarboxylase
10 <130> FILE REFERENCE: 028723-385
12 <140> CURRENT APPLICATION NUMBER: US 10/641,149
13 <141> CURRENT FILING DATE: 2003-08-15
15 <150> PRIOR APPLICATION NUMBER: US 07/586,536
16 <151> PRIOR FILING DATE: 1990-09-12
18 <160> NUMBER OF SEQ ID NOS: 8
20 <170> SOFTWARE: FastSEQ for Windows Version 4.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 60
24 <212> TYPE: PRT
25 <213> ORGANISM: Felis
27 <400> SEQUENCE: 1
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30 Lys Met Arg Glu Ile Val Gly Trp Ser Ser Lys Asp Gly Asp Gly Ile
31             20                  25                  30
32 Phe Ser Pro Gly Gly Ala Ile Ser Asn Met Tyr Ser Ile Met Ala Ala
33             35                  40                  45
34 Arg Tyr Lys Phe Phe Pro Glu Val Lys Thr Lys Gly
35      50                  55                  60
38 <210> SEQ ID NO: 2
39 <211> LENGTH: 53
40 <212> TYPE: PRT
41 <213> ORGANISM: Mus musculus
43 <400> SEQUENCE: 2
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46 Ile Gly Trp Pro Gly Gly Ser Asp Gly Ile Phe Ser Pro Gly Gly Ala
47             20                  25                  30
48 Ile Ser Asn Tyr Ala Met Leu Ile Ala Arg Tyr Lys Met Phe Pro Glu
49             35                  40                  45
50 Val Lys Glu Lys Gly
51      50
54 <210> SEQ ID NO: 3
55 <211> LENGTH: 1966
56 <212> TYPE: DNA
57 <213> ORGANISM: Mus musculus
59 <400> SEQUENCE: 3
60 gggcgtgcgg ggtcgagccg aagcagcttg cccgcagcca ctcggaggcg accagcgcca 60
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61 gactagcaga acccatggca tctccgggct ctggcttttg gtccttcgga tctgaagatg 120
62 gctctgggga tcctgagaac ccgggaacag cgagagcctg gtgccaggtg gcccaaaagt 180
63 tcacgggcgg catcggaaac aagctatgcg ctctgctcta cggagactct gagaagccag 240
64 cagagagcgg cgggagcgtg acctcgcggg ccgccactcg gaaggtcgcc tgcacctgtg 300
65 accaaaaacc ctgcagctgc cccaaaggag atgtcaatta tgcacttctc cacgcaacag 360
66 acctgctgcc agcctgtgaa ggagaaaggc ccactctcgc atttctgcaa gatgtaatga 420
67 acattttgct tcagtacgtg gtgaaaagtt ttgatagatc aactaaagtg attgatttcc 480
68 attaccccaa tgagcttctt caagagtata attgggaatt ggcagaccaa ccgcaaaatc 540
69 tggaggaaat tttgacgcac tgccaaacaa ctctaaaata tgcgattaaa acagggcatc 600
70 cccgatattt taatcagctg tctaccggat tggatatggt tggattagca gcagattggt 660
71 tgacatcaac agcaaacacg aacatgttta cctatgagat cgcccctgta tttgtactac 720
72 tggaatatgt gacactaaag aaaatgaggg aaatcattgg ctggccagga ggctctggcg 780
73 atggaatctt ttctcctggt ggtgccatct ccaacatgta cgccatgctc attgcccgct 840
74 ataagatgtt tccagaagtc aaggaaaagg ggatggcggc ggtgcccagg ctcatcgcat 900
75 tcacgtcaga gcatagtcac ttttctctca agaagggagc tgcagccttg gggatcggaa 960
76 cagacagcgt gattctgatt aaatgtgatg agagagggaa aatgatccca tctgaccttg 1020
77 aaagaagaat ccttgaagtc aaacagaaag gatttgttcc tttcctggtg agtgccacag 1080
78 ctggaaccac tgtgtacggg gcttttgatc ctctcttggc tgtagctgac atctgcaaaa 1140
79 aatataagat ctggatgcat gtggatgctg cttggggtgg agggttactg atgtctcgga 1200
80 aacacaagtg gaagctgaac ggtgtggaga gggccaactc tgtgacatgg aatccccaca 1260
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87 tggaagacaa tgaagagaga atgagccgcc tctcaaaggt ggcgccagtg attaaagcca 1680
88 gaatgatgga gtatgggacc acaatggtca gctaccaacc cttaggagat aaggtcaact 1740
89 tcttccgcat ggtcatctca aaccctgcag caactcacca agacattgac ttcctcattg 1800
90 aagaaatcga acgcctggga caagatttgt aatcactttg ctcaccaaac tttcagttct 1860
91 ctaggtagac agctaagttg tcacaaactg tgtaaatgta tttgtagttt gttccagagt 1920
92 aattctattt ctatatcgtg gtgtcacagt agagtccagt ttaaaa       1966
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94 <210> SEQ ID NO: 4
95 <211> LENGTH: 1758
96 <212> TYPE: DNA
97 <213> ORGANISM: Mus musculus
99 <220> FEATURE:
100 <221> NAME/KEY: CDS
101 <222> LOCATION: (1)...(1758)
103 <400> SEQUENCE: 4

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105 Met Ala Ser Pro Gly Ser Gly Phe Trp Ser Phe Gly Ser Glu Asp Gly
106 1               5                   10                  15
108 tct ggg gat cct gag aac ccg gga aca gcg aga gcc tgg tgc cag gtg    96
109 Ser Gly Asp Pro Glu Asn Pro Gly Thr Ala Arg Ala Trp Cys Gln Val
110             20                  25                  30
112 gcc caa aag ttc acg ggc ggc atc gga aac aag cta tgc gct ctg ctc   144
113 Ala Gln Lys Phe Thr Gly Gly Ile Gly Asn Lys Leu Cys Ala Leu Leu
114         35                  40                  45
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116 tac gga gac tct gag aag cca gca gag agc ggc ggg agc gtg acc tcg    192
117 Tyr Gly Asp Ser Glu Lys Pro Ala Glu Ser Gly Gly Ser Val Thr Ser
118      50              55              60
120 cgg gcc gcc act cgg aag gtc gcc tgc acc tgt gac caa aaa ccc tgc    240
121 Arg Ala Ala Thr Arg Lys Val Ala Cys Thr Cys Asp Gln Lys Pro Cys
122  65              70              75              80
124 agc tgc ccc aaa gga gat gtc aat tat gca ctt ctc cac gca aca gac    288
125 Ser Cys Pro Lys Gly Asp Val Asn Tyr Ala Leu Leu His Ala Thr Asp
126              85              90              95
128 ctg ctg cca gcc tgt gaa gga gaa agg ccc act ctc gca ttt ctg caa    336
129 Leu Leu Pro Ala Cys Glu Gly Glu Arg Pro Thr Leu Ala Phe Leu Gln
130             100          .      105             110
132 gat gta atg aac att ttg ctt cag tac gtg gtg aaa agt ttt gat aga    384
133 Asp Val Met Asn Ile Leu Leu Gln Tyr Val Val Lys Ser Phe Asp Arg
134     115             120             125
136 tca act aaa gtg att gat ttc cat tac ccc aat gag ctt ctt caa gag    432
137 Ser Thr Lys Val Ile Asp Phe His Tyr Pro Asn Glu Leu Leu Gln Glu
138     130             135             140
140 tat aat tgg gaa ttg gca gac caa ccg caa aat ctg gag gaa att ttg    480
141 Tyr Asn Trp Glu Leu Ala Asp Gln Pro Gln Asn Leu Glu Glu Ile Leu
142 145             150             155             160
144 acg cac tgc caa aca act cta aaa tat gcg att aaa aca ggg cat ccc    528
145 Thr His Cys Gln Thr Thr Leu Lys Tyr Ala Ile Lys Thr Gly His Pro
146             165             170             175
148 cga tat ttt aat cag ctg tct acc gga ttg gat atg gtt gga tta gca    576
149 Arg Tyr Phe Asn Gln Leu Ser Thr Gly Leu Asp Met Val Gly Leu Ala
150             180             185             190
152 gca gat tgg ttg aca tca aca gca aac acg aac atg ttt acc tat gag    624
153 Ala Asp Trp Leu Thr Ser Thr Ala Asn Thr Asn Met Phe Thr Tyr Glu
154     195             200             205
156 atc gcc cct gta ttt gta cta ctg gaa tat gtg aca cta aag aaa atg    672
157 Ile Ala Pro Val Phe Val Leu Leu Glu Tyr Val Thr Leu Lys Lys Met
158     210             215             220
160 agg gaa atc att ggc tgg cca gga ggc tct ggc gat gga atc ttt tct    720
161 Arg Glu Ile Ile Gly Trp Pro Gly Gly Ser Gly Asp Gly Ile Phe Ser
162 225             230             235             240
164 cct ggt ggt gcc atc tcc aac atg tac gcc atg ctc att gcc cgc tat    768
165 Pro Gly Gly Ala Ile Ser Asn Met Tyr Ala Met Leu Ile Ala Arg Tyr
166             245             250             255
168 aag atg ttt cca gaa gtc aag gaa aag ggg atg gcg gcg gtg ccc agg    816
169 Lys Met Phe Pro Glu Val Lys Glu Lys Gly Met Ala Ala Val Pro Arg
170             260             265             270
172 ctc atc gca ttc acg tca gag cat agt cac ttt tct ctc aag aag gga    864
173 Leu Ile Ala Phe Thr Ser Glu His Ser His Phe Ser Leu Lys Lys Gly
174     275         .       280             285
176 gct gca gcc ttg ggg atc gga aca gac agc gtg att ctg att aaa tgt    912
177 Ala Ala Ala Leu Gly Ile Gly Thr Asp Ser Val Ile Leu Ile Lys Cys
178     290             295             300
180 gat gag aga ggg aaa atg atc cca tct gac ctt gaa aga aga atc ctt    960
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181 Asp Glu Arg Gly Lys Met Ile Pro Ser Asp Leu Glu Arg Arg Ile Leu
182 305           310           315           320
184 gaa gtc aaa cag aaa gga ttt gtt cct ttc ctg gtg agt gcc aca gct    1008
185 Glu Val Lys Gln Lys Gly Phe Val Pro Phe Leu Val Ser Ala Thr Ala
186           325           330           335
188 gga acc act gtg tac ggg gct ttt gat cct ctc ttg gct gta gct gac    1056
189 Gly Thr Thr Val Tyr Gly Ala Phe Asp Pro Leu Leu Ala Val Ala Asp
190           340           345           350
192 atc tgc aaa aaa tat aag atc tgg atg cat gtg gat gct gct tgg ggt    1104
193 Ile Cys Lys Lys Tyr Lys Ile Trp Met His Val Asp Ala Ala Trp Gly
194           355           360           365
196 gga ggg tta ctg atg tct cgg aaa cac aag tgg aag ctg aac ggt gtg    1152
197 Gly Gly Leu Leu Met Ser Arg Lys His Lys Trp Lys Leu Asn Gly Val
198           370           375           380
200 gag agg gcc aac tct gtg aca tgg aat ccc cac aag atg atg ggt gtc    1200
201 Glu Arg Ala Asn Ser Val Thr Trp Asn Pro His Lys Met Met Gly Val
202 385           390           395           400
204 ccc ttg caa tgt tcg gct ctc ctg gtc aga gag gag gga ctg atg cag    1248
205 Pro Leu Gln Cys Ser Ala Leu Leu Val Arg Glu Glu Gly Leu Met Gln
206           405           410           415
208 agc tgc aac cag atg cat gct tcc tac ctc ttt cag caa gat aag cac    1296
209 Ser Cys Asn Gln Met His Ala Ser Tyr Leu Phe Gln Gln Asp Lys His
210           420           425           430
212 tat gac ctg tcc tat gac acg gga gac aag gcc ttg cag tgt gga cgc    1344
213 Tyr Asp Leu Ser Tyr Asp Thr Gly Asp Lys Ala Leu Gln Cys Gly Arg
214           435           440           445
216 cac gtc gat gtc ttt aaa tta tgg ctc atg tgg aga gca aag ggg act    1392
217 His Val Asp Val Phe Lys Leu Trp Leu Met Trp Arg Ala Lys Gly Thr
218 450           455           460
220 act gga ttt gaa gct cac att gat aag tgt ttg gag ctg gca gag tat    1440
221 Thr Gly Phe Glu Ala His Ile Asp Lys Cys Leu Glu Leu Ala Glu Tyr
222 465           470           475           480
224 tta tac aat atc att aaa aac cga gaa gga tat gaa atg gtg ttc gat    1488
225 Leu Tyr Asn Ile Ile Lys Asn Arg Glu Gly Tyr Glu Met Val Phe Asp
226           485           490           495
228 ggg aag cct cag cac aca aat gtc tgc ttc tgg ttt gta cct cct agt    1536
229 Gly Lys Pro Gln His Thr Asn Val Cys Phe Trp Phe Val Pro Pro Ser
230           500           505           510
232 ttg cga gtt ctg gaa gac aat gaa gag aga atg agc cgc ctc tca aag    1584
233 Leu Arg Val Leu Glu Asp Asn Glu Glu Arg Met Ser Arg Leu Ser Lys
234           515           520           525
236 gtg gcg cca gtg att aaa gcc aga atg atg gag tat ggg acc aca atg    1632
237 Val Ala Pro Val Ile Lys Ala Arg Met Met Glu Tyr Gly Thr Thr Met
238 530           535           540
240 gtc agc tac caa ccc tta gga gat aag gtc aac ttc ttc cgc atg gtc    1680
241 Val Ser Tyr Gln Pro Leu Gly Asp Lys Val Asn Phe Phe Arg Met Val
242 545           550           555           560
244 atc tca aac cct gca gca act cac caa gac att gac ttc ctc att gaa    1728
245 Ile Ser Asn Pro Ala Ala Thr His Gln Asp Ile Asp Phe Leu Ile Glu
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248 gaa atc gaa cgc ctg gga caa gat ttg taa                          1758
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254 <211> LENGTH: 585
255 <212> TYPE: PRT
256 <213> ORGANISM: Mus musculus
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261 Ser Gly Asp Pro Glu Asn Pro Gly Thr Ala Arg Ala Trp Cys Gln Val
262               20                  25                  30
263 Ala Gln Lys Phe Thr Gly Gly Ile Gly Asn Lys Leu Cys Ala Leu Leu
264           35                  40                  45
265 Tyr Gly Asp Ser Glu Lys Pro Ala Glu Ser Gly Gly Ser Val Thr Ser
266      50                  55                  60
267 Arg Ala Ala Thr Arg Lys Val Ala Cys Thr Cys Asp Gln Lys Pro Cys
268 65                  70                  75                  80
269 Ser Cys Pro Lys Gly Asp Val Asn Tyr Ala Leu Leu His Ala Thr Asp
270               85                  90                  95
271 Leu Leu Pro Ala Cys Glu Gly Glu Arg Pro Thr Leu Ala Phe Leu Gln
272           100                 105                 110
273 Asp Val Met Asn Ile Leu Leu Gln Tyr Val Val Lys Ser Phe Asp Arg
274           115                 120                 125
275 Ser Thr Lys Val Ile Asp Phe His Tyr Pro Asn Glu Leu Leu Gln Glu
276      130                 135                 140
277 Tyr Asn Trp Glu Leu Ala Asp Gln Pro Gln Asn Leu Glu Glu Ile Leu
278 145                 150                 155                 160
279 Thr His Cys Gln Thr Thr Leu Lys Tyr Ala Ile Lys Thr Gly His Pro
280               165                 170                 175
281 Arg Tyr Phe Asn Gln Leu Ser Thr Gly Leu Asp Met Val Gly Leu Ala
282           180                 185                 190
283 Ala Asp Trp Leu Thr Ser Thr Ala Asn Thr Asn Met Phe Thr Tyr Glu
284           195                 200                 205
285 Ile Ala Pro Val Phe Val Leu Leu Glu Tyr Val Thr Leu Lys Lys Met
286      210                 215                 220
287 Arg Glu Ile Ile Gly Trp Pro Gly Gly Ser Gly Asp Gly Ile Phe Ser
288 225                 230                 235                 240
289 Pro Gly Gly Ala Ile Ser Asn Met Tyr Ala Met Leu Ile Ala Arg Tyr
290               245                 250                 255
291 Lys Met Phe Pro Glu Val Lys Glu Lys Gly Met Ala Ala Val Pro Arg
292           260                 265                 270
293 Leu Ile Ala Phe Thr Ser Glu His Ser His Phe Ser Leu Lys Lys Gly
294           275                 280                 285
295 Ala Ala Ala Leu Gly Ile Gly Thr Asp Ser Val Ile Leu Ile Lys Cys
296      290                 295                 300
297 Asp Glu Arg Gly Lys Met Ile Pro Ser Asp Leu Glu Arg Arg Ile Leu
298 305                 310                 315                 320
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VERIFICATION SUMMARY
PATENT APPLICATION: US/10/641,149

DATE: 03/30/2005
TIME: 10:17:05

Input Set : **A:\028723-385.txt**
Output Set: **N:\CRF4\03302005\J641149.raw**